Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

Claim 1 (previously presented): A method for identifying a transcribed region of interest of a genome comprising:

a) Hybridizing a plurality of nucleic acid probes with a nucleic acid sample, wherein said nucleic acid sample comprises transcripts from said genome, wherein said probes are targeting an area of said genome; and

b) Identifying said transcribed region as a region of said genome where hybridization of all consecutive probes targeting said region are above a threshold value.

Claim 2 (original): The method of claim 1 wherein said probes are oligonucleotides.

Claim 3 (original): The method of claim 3 wherein said oligonucleotides are immobilized on a substrate.

Claim 4 (original): The method of claim 1 wherein said threshold is non-specific binding.

Claim 5 (currently amended): The method of claim 4 wherein said non-specific binding is measured using a probe designed to contain containing at least one mismatched base.

1 Claim 6 (currently amended): The method of claim 1 further
2 comprising:

3

4   c) Identifying a sub-region wherein hybridization of
5 said probes targeting said sub-region ~~sub-regions~~ is similar
6 ~~and~~, thereby indicating said sub-region as said transcribed
7 region.

1 Claim 7 (original): The method of claim 6 wherein said
2 genome is from a prokaryote.

1 Claim 8 (original): The method of claim 7 wherein said
2 transcribed region is an operon.

1 Claim 9 (currently amended): The method of ~~claim 8~~ claim 7
2 wherein said prokaryote is bacteria.

   Claims 10-14 (canceled)